

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: May 7, 2002, 12:08:53 ; Search time 19.81 Seconds
(without alignments)
262.817 Million cell updates/sec

Title: US-09-772-103-10
Perfect score: 742
Sequence: 1 MAVLVFLCLVAPPSCVLSQ.....MKRGVAMDYWGQGLTVTVSS 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
al number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	506	68.2	144	1 HV43_MOUSE	P01819 mus musculus
2	475	64.0	116	1 HV45_MOUSE	P01821 mus musculus
3	464	62.5	115	1 HV44_MOUSE	P01820 mus musculus
4	415	55.9	135	1 HV02_XENLA	P06957 xenopus lae
5	414.5	55.9	146	1 HV21_HUMAN	P03331 homo sapien
6	390.5	52.6	137	1 HV46_MOUSE	P01822 mus musculus
7	379	51.1	117	1 HV26_HUMAN	P01824 homo sapien
8	376	50.7	129	1 HV2F_HUMAN	P01825 homo sapien
9	366	49.3	136	1 HV01_XENLA	P20956 xenopus lae
10	361	48.7	116	1 HV61_MOUSE	P18532 mus musculus
11	352	47.4	116	1 HV60_MOUSE	P18531 mus musculus
12	342.5	46.2	147	1 HV2H_HUMAN	P04438 homo sapien
13	341.5	46.0	120	1 HV2B_HUMAN	P01815 homo sapien
14	339	45.7	121	1 HV3J_HUMAN	P01771 homo sapien
15	332.5	44.8	126	1 HV3K_HUMAN	P01772 homo sapien
16	332	44.7	113	1 HV47_MOUSE	P01823 mus musculus
17	329.5	44.4	122	1 HV3G_HUMAN	P01768 homo sapien
18	325	43.8	119	1 HV2C_HUMAN	P01816 homo sapien
19	324	43.7	125	1 HV2D_HUMAN	P01817 homo sapien
20	324	43.7	136	1 HV2C_RABIT	P01829 oryctolagus
21	323.5	43.6	117	1 HV62_MOUSE	P18533 mus musculus
22	321.5	43.3	136	1 HV16_MOUSE	P01783 mus musculus
23	316.5	42.7	122	1 HV3H_HUMAN	P01769 homo sapien
24	310	41.8	121	1 HV3H_HUMAN	P01818 homo sapien
25	309	41.6	140	1 HV02_MOUSE	P01746 mus musculus
26	308.5	41.6	114	1 HV2A_RABIT	P01827 oryctolagus
27	307.5	41.4	119	1 HV2B_MOUSE	P01828 oryctolagus
28	306	41.2	117	1 HV2B_MOUSE	P01765 mus musculus
29	305	41.1	115	1 HV3D_HUMAN	P01805 rattus norv
30	305	41.1	142	1 HV01_RAT	P01763 mus musculus
31	304.5	41.0	114	1 HV3B_HUMAN	P01807 mus musculus
32	304.5	41.0	119	1 HV37_MOUSE	P01814 homo sapien
33	304.5	41.0	126	1 HV2A_HUMAN	

34	304.5	41.0	137	1 HV11_MOUSE	P01755 mus musculus
35	302.5	40.8	139	1 HV07_MOUSE	P01751 mus musculus
36	302	40.7	116	1 HV05_CARAG	P0181 carassius a
37	302	40.7	119	1 HV31_HUMAN	P01770 homo sapien
38	299	40.3	119	1 HV3L_HUMAN	P01773 homo sapien
39	297	40.0	117	1 HV42_MOUSE	P01812 mus musculus
40	296	39.9	115	1 HV3F_HUMAN	P01767 homo sapien
41	295.5	39.8	116	1 HV3T_HUMAN	P01781 homo sapien
42	294	39.6	116	1 HV48_MOUSE	P03980 mus musculus
43	293.5	39.6	119	1 HV3P_HUMAN	P01777 homo sapien
44	292.5	39.4	116	1 HV1A_RABIT	P01826 oryctolagus
45	292	39.4	120	1 HV03_MOUSE	P01747 mus musculus

ALIGNMENTS

RESULT HV43_MOUSE 1
ID HV43_MOUSE STANDARD; PRT; 144 AA.
AC P01819; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG HEAVY CHAIN V REGION MOPC 141 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa F., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683(1980).
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.

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or send an email to license@isb-sib.ch).
CC EMBL: J00491; AAA38121.1; -;
DR EMBL: V00768; CAA24149.1; -;
PIR: A02094; G2MS14.
DR InterPro: IPR003006; Iq_MHC.
DR Pfam: PF00047; Iq; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 19
FT NON_TER 20 144 IG HEAVY CHAIN V REGION MOPC 141.
FT SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 68.2%; Score 506; DB 1; Length 144;
Best Local Similarity 67.4%; Pred. No. 1.6e-43;
Matches 97; Conservative 15; Mismatches 30; Indels 2; Gaps 1;

QY	1	MAVLVFLCLVAPPSCVLSQVQLQESGPGLVKPSQSLTCTCTVSGFSLTGYGVWRQPP	60
DB	1	MAVLALLFLCLATFPSCILSQVQLKESGPGLVAPSOSSLITCTVSGFSLTGYGVWRQPP	60
QY	61	GRGLEWLVGIWAGTNTYNSALMSRLTISKDTSKNQVSKLSSVTAADTAVYYCARGP	118
DB	61	GRGLEWLVGIWAGTNTYNSALMSRLTISKDTSKNQVSKLSSVTAADTAVYYCARGP	118

us-09-772-103-10-1.rsp

Mon Jul 1 16:28:04 2002

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RP MEDLINE=81012133; PubMed=6774258;
RX Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RA "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683(1980).
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CC -----
CC EMBL; V00767; GAA24148.1; -.
DR PIR; A02095; HVMS14.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 115 IG HEAVY CHAIN V REGION PJ14.
FT NON_TER 115 115
FT SEQUENCE 115 AA; 12447 MW; 7569DD4A4843D500 CRC64;
SQ
Query Match 62.5%; Score 464; DB 1; Length 115;
Best Local Similarity 75.7%; Pred. No. 1.8e-39;
Matches 87; Conservative 12; Mismatches 16; Indels 0; Gaps 0;
Qy 1 MAVLVFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGIVYVWRQPP 60
Db 1 MAVLALLFCLVTFPESCILSQVLKESGPGLVAPQSLSITCTVSGFSLGIVGVNWRQPP 60
Qy 61 GKGLEWLVGIWAGGTNTNYSALMSRLTISKDTNKNQVSLKSSVTAADTAVYKCA 115
Db 61 GKGLEWLVGMINGDGTNDYNSALMSRLTISKDTNKNQVSLKSSVTAADTAVYKCA 115
Qy 61 GKGLEWLVGMINGDGTNDYNSALMSRLTISKDTNKNQVSLKSSVTAADTAVYKCA 115
Db 61 GKGLEWLVGMINGDGTNDYNSALMSRLTISKDTNKNQVSLKSSVTAADTAVYKCA 115
RESULT 4
HV02_XENLA STANDARD; PRT; 135 AA.
ID HV02_XENLA
AC P20957;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION XIG14 PRECURSOR (FRAGMENT).
OS Xenopus laevis (African clawed frog);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis Igm deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains";
RT Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
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CC -----
CC EMBL; J03632; AAA49791.1; -.
DR PIR; B31933; B31933.

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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN <1 18
FT CHAIN 19 135
FT NON_TER 135
FT NON_TER 135
SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732B CRC64;

Query Match
Best Local Similarity 55.9%; Score 415; DB 1; Length 135;
Matches 78; Conservative 24; Mismatches 31; Indels 6; Gaps 2;
QY 4 LVFLCLVAFSCVLSQVQLQESGPGGLVPSQTLSTCTVSGLSYGVYVWVQPPGKG 63
DB 3 IIFIFMFPSFCSLSQT-LQESGPGVTKPSESRLTCTVSGFELSSYHHHWIRQPPGKG 61
64 LEWLGVIWAGGTTNYSALMSRLTISKDTSKNOVSLKLSVTAADTAVVYVCARGPPHAMM 123
DB 62 LEWLGVIATGSGTAIDSLANRVTITDNGKKQVYLMNGMEVKDTAMYCAR-----EY 116
QY 124 KRGYADYWGQGLTVTVSS 142
DB 117 ASGYNFDYWGQGLTVTVTS 135

RESULT 5
ID HV21_HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 05, Created)
DT 01-JAN-1988 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-II REGION ARH-77 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT repeat sequence in 5' flanking region.;
RL Gene 33181-189(1985).
RN [2]
RP HSSP; P01825; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19
FT DOMAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
FT DOMAIN 20 117 V SEGMENT.
FT DOMAIN 118 127 D SEGMENT.
FT DOMAIN 128 146 J SEGMENT.
FT DISULFID 42 115 BY SIMILARITY.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match
Best Local Similarity 55.9%; Score 414.5; DB 1; Length 146;
Matches 86; Conservative 13; Mismatches 23; Indels 11; Gaps 2;
QY 17 VLSQVQLQESGPGGLVPSQTLSTCTVSGLSYGVYVWVQPPGKGLEWLVWAGGTT 76
DB 18 VLSQVQLQWAGLVPKSETLSLTCAVEGSGFSGYVSWIRQPPGRLGLEWVINS 77

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QY 77 NYSALMSRLTISKDTSKNOVSLKLSVTAADTAVVYVCARGPPHAMMKG-----YAM 129
DB 78 NYKTSLSKRVITSLDTSKNLFSKLSVTAADTAVVYVCARG-----LLRGWNVDVYVGM 133
QY 130 DYWGQGLTVTVSS 142
DB 134 DVWGQGLTVTVSS 146

RESULT 6
ID HV46_MOUSE STANDARD; PRT; 137 AA.
AC P01822;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 315 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89238351; PubMed=2497341;
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RL Mol. Immunol. 26:431-434(1989).
RN [2]
RP SEQUENCE OF 1-31.
RX MEDLINE=78094475; PubMed=414225;
RA Jilka R.L., Pestka S.;
RT "Amino acid sequence of the precursor region of MOPC-315 mouse
RL immunoglobulin heavy chain.";
RN [3]
RP SEQUENCE OF 1-21.
RX MEDLINE=79148758; PubMed=428562;
RA Schechter I., Wolf O., Zemell R., Burstein Y.;
RT "Structure and function of immunoglobulin genes and precursors.";
RN [4]
RP SEQUENCE OF 19-136.
RX MEDLINE=74170779; PubMed=4524622;
RA Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
RT chain of a mouse myeloma protein with anti-hapten activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
RN [5]
RP REVISION TO 53.
RX MEDLINE=77244979; PubMed=268248;
RA Hood L., Margolies M.N., Givol D., Zakut R.;
RL Unpublished results, cited by:
RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
CC Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
CC -!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
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CC -----
DR EMBL; M27638; AAA61337.1; -
DR EMBL; X07880; CAA30727.1; -
DR PIR; P01012; AVMS35.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
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us-09-772-103-10.rsp

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Immunoglobulin V region; Signal.

1 18 IG HEAVY CHAIN V REGION MOPC 315.
 19 137 FRAMEWORK 1.
 20 48 COMPLEMENTARITY-DETERMINING 1.
 21 54 FRAMEWORK 2.
 22 68 COMPLEMENTARITY-DETERMINING 2.
 23 84 FRAMEWORK 3.
 24 85 COMPLEMENTARITY-DETERMINING 3.
 25 116 FRAMEWORK 4.
 26 126 FRAMEWORK 4.
 27 137 BY SIMILARITY.
 28 114 G -> GG (IN REF. 1; CAA30727).
 29 15 G -> H (IN REF. 2).
 30 15 GY -> YG (IN REF. 4).
 31 78 N -> D (IN REF. 4).
 32 102 MISSING (IN REF. 4).
 33 123
 34 137
 35 137 AA; 15399 MW; FB3828304C2B81DC CRC64;
 36 137 AA; 12790 MW; 2DA47B509562D237 CRC64;
 37 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
 38 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
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 154 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
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 191 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
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 197 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
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 199 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
 200 117 AA; 12790 MW; 2DA47B509562D237 CRC64;

Query Match 51.1%; Score 379; DB 1; Length 117;
 Best Local Similarity 62.6%; Pred. No. 5.3e-31;
 Matches 77; Conservative 19; Mismatches 21; Indels 6; Gaps 2;

20 QVQLQESGPGVLRPSQTLSTCTVSGFSLTSYGVYVVRQPPGKGLWLVWAGGTTN 79
 1 QVQLQESGPGVLRPSQTLSTCTVSGFSLTSYGVYVVRQPPGKGLWLVWAGGTTN 79
 80 SALMSRTISKDTSKNOVSLKSLSVTAADTAVYYCARGPPHAMMKRGYAMDYWGQTLVT 139
 61 TPLRSRVTLVDTSKNOVSLKSLSVTAADTAVYYCARN-----LIAG-CIDVWGQSLVT 114
 140 VSS 142
 115 VSS 117

RESULT 8
 HV2F_HUMAN STANDARD; PRT; 129 AA.
 ID HV2F_HUMAN
 AC P01824;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-II REGION WAH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 [1]
 RN SEQUENCE.
 RP MEDLINE=82222235; PubMed=6806818;
 RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
 RT "Complete amino acid sequence of the delta heavy chain of human
 immunoglobulin D.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
 CC PROTEIN.
 CC PIR; A02099; D2HWA.
 DR HSP; P01825; 7FAB.
 DR GlycosuiteDB; P01824;
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR Immunoglobulin V region.
 KW NON_TER 129 129
 FT SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Immunoglobulin V region; Signal.

1 18 IG HEAVY CHAIN V REGION MOPC 315.
 19 137 FRAMEWORK 1.
 20 48 COMPLEMENTARITY-DETERMINING 1.
 21 54 FRAMEWORK 2.
 22 68 COMPLEMENTARITY-DETERMINING 2.
 23 84 FRAMEWORK 3.
 24 85 COMPLEMENTARITY-DETERMINING 3.
 25 116 FRAMEWORK 4.
 26 126 FRAMEWORK 4.
 27 137 BY SIMILARITY.
 28 114 G -> GG (IN REF. 1; CAA30727).
 29 15 G -> H (IN REF. 2).
 30 15 GY -> YG (IN REF. 4).
 31 78 N -> D (IN REF. 4).
 32 102 MISSING (IN REF. 4).
 33 123
 34 137
 35 137 AA; 15399 MW; FB3828304C2B81DC CRC64;
 36 137 AA; 12790 MW; 2DA47B509562D237 CRC64;
 37 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
 38 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
 39 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
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 73 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
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 113 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
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 120 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
 121 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
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Query Match
Best Local Similarity 50.78; Score 376; DB 1; Length 129;
Matches 77; Conservative 18; Mismatches 28; Indels 6; Gaps 3;

QY 20 QVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVY--WVROPKGLWGLVWVWAGGTTN 77
Db 1 RLQDQESGPGVLPKPSQTLSTCTVSGFSLTSYGVY--WVROPKGLWGLVWVWAGGTTN 77
QY 78 YNSALMSRLTISKDTKNOVSLKSLVTAADTAVYYCAR--PPHAMMKRGY--AMDYWG 133
Db 61 YNPSLRGRVTISVDTSRNFSLNLSMSAADTAMTYCARGNPPYDIDGTGSDGDIDVWG 120
QY 134 QGLTVTVSS 142
Db 121 QGLTVTVSS 129

RESULT 9
HV01_XENLA
HV01_XENLA STANDARD; PRT; 136 AA.
P20956;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION XIG8 PRECURSOR (FRAGMENT).
Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
MEDLINE=88176921; PubMed=2451244;
Schwager J., Mikoryak C.A., Steiner L.A.;
"Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
from cDNA sequence: implications for evolution of immunoglobulin
domains.";
Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
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EMBL; M20484; AAA49774.1; ALT_TERM.
PIR; A31933; A31933
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig_v.
SMART; SM00406; Igv; 1.
Immunoglobulin V region; Signal.
NON_TER 1
CHAIN <1 18
FT CHAIN 19 136 IG HEAVY CHAIN V REGION XIG8.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15123 MW; 3141838981441963 CRC64;

Query Match
Best Local Similarity 49.38; Score 366; DB 1; Length 136;
Matches 74; Conservative 23; Mismatches 35; Indels 6; Gaps 4;

QY 6 LFLCLVAF-PSCVLSQVQLQESGPGGLVKPSQTLSTCTVSGFSLTSYGVYVWROPKGL 64
Db 4 IFVIFMFPSFCLISQT-LQESGPGVLPKPSQTLSTCTVSGFSLTSYGVYVWROPKGL 64
QY 65 EWLGVIWAGTTNYSALMSRLTISKDTKNOVSLKSLVTAADTAVYYCARGPPEHAMMK 124
Db 63 EWIGVVRDGTGSAIDSLKRNVTITKDKNGKKOVLQMGMEVKTAMTYCT---STLAGT 119

Query Match
Best Local Similarity 59.78; Score 376; DB 1; Length 129;
Matches 77; Conservative 18; Mismatches 28; Indels 6; Gaps 3;

QY 20 QVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVY--WVROPKGLWGLVWVWAGGTTN 77
Db 1 RLQDQESGPGVLPKPSQTLSTCTVSGFSLTSYGVY--WVROPKGLWGLVWVWAGGTTN 77
QY 78 YNSALMSRLTISKDTKNOVSLKSLVTAADTAVYYCAR--PPHAMMKRGY--AMDYWG 133
Db 61 YNPSLRGRVTISVDTSRNFSLNLSMSAADTAMTYCARGNPPYDIDGTGSDGDIDVWG 120
QY 134 QGLTVTVSS 142
Db 121 QGLTVTVSS 129

RESULT 9
HV01_XENLA
HV01_XENLA STANDARD; PRT; 136 AA.
P20956;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION XIG8 PRECURSOR (FRAGMENT).
Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
MEDLINE=88176921; PubMed=2451244;
Schwager J., Mikoryak C.A., Steiner L.A.;
"Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
from cDNA sequence: implications for evolution of immunoglobulin
domains.";
Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
-----
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or send an email to license@isb-sib.ch).
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EMBL; M20484; AAA49774.1; ALT_TERM.
PIR; A31933; A31933
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig_v.
SMART; SM00406; Igv; 1.
Immunoglobulin V region; Signal.
NON_TER 1
CHAIN <1 18
FT CHAIN 19 136 IG HEAVY CHAIN V REGION XIG8.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15123 MW; 3141838981441963 CRC64;

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QY 125 RGYAMYWGQGLTVTVSS 142
Db 120 AGY-FEHWGQGLTVTVSS 136

RESULT 10
HV61_MOUSE
HV61_MOUSE STANDARD; PRT; 116 AA.
AC P18532;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 1B43 PRECURSOR.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=BALE/CJ;
MEDLINE=89279149; PubMed=2499654;
Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
DR PIR; JTO508; HVMSIB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION 1B43.
FT DOMAIN 19 48 FRAMEWORK 1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 54 67 FRAMEWORK 2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 85 116 FRAMEWORK 3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;

Query Match
Best Local Similarity 48.7%; Score 361; DB 1; Length 116;
Matches 72; Conservative 17; Mismatches 26; Indels 2; Gaps 2;

QY 1 MAVLVFLCLVAFPPSCVLSQVQLQESGPGGLVKPSQTLSTCTVSGFSLTS-YGVYVWROP 59
Db 1 MRVLILLCLLFTAPPG-ILSDVQLQESGPGGLVKPSQSLTCTVGTGYSYSHHWIRQF 59
QY 60 PGKGLWGLVWAGTTNYSALMSRLTISKDTKNOVSLKSLVTAADTAVYYCAR 116
Db 60 POKLEWGYIHYSGNTSYNPSLKSRLTSDTSKQNFLOLNSVTVDATYYCAR 116

RESULT 11
HV60_MOUSE
HV60_MOUSE STANDARD; PRT; 116 AA.
AC P18531;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION M315 PRECURSOR.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=BALE/CJ;
MEDLINE=89279149; PubMed=2499654;

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us-09-772-103-10.rsp

Mon Jul 1 16:28:04 2002

RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 RL the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 DR PIR: JTO509; HVMS31.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_v.
 DR SMART: SM00406; IgV; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 18
 FT CHAIN 19 116 IG HEAVY CHAIN V REGION M315.
 FT DOMAIN 19 48 FRAMEWORK 1.
 FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 54 67 FRAMEWORK 2.
 FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 85 116 FRAMEWORK 3.
 FT DISULFID 40 114 BY SIMILARITY.
 FT NON_TER 116 116
 FT SEQUENCE 116 AA; 13095 MW; 45G2E03E53DC9E10 CRC64;
 Query Match 47.4%; Score 352; DB 1; Length 116;
 Best Local Similarity 61.9%; Pred. No. 2.6e-28;
 Matches 73; Conservative 16; Mismatches 25; Indels 4; Gaps 3;
 QY 1 MAVLVFLCLVAPPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYG--VYVVRQ 58
 DB 1 MKVLSLLYLLTAIPG-ILSDVQLQESGPGLVKPSQSLSTCTVSGFSLTSYG--VYVVRQ 58
 QY 59 PPGKLEWLVGVIWAGGTTNNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116
 DB 59 PPGKLEWLVGVIWAGGTTNNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116
 QY 59 PPGKLEWLVGVIWAGGTTNNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116
 DB 59 PPGKLEWLVGVIWAGGTTNNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116
 RESULT 12
 HV2H_HUMAN STANDARD; PRT; 147 AA.
 ID HV2H_HUMAN
 AC P0438; (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-II REGION SESS PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=84298107; PubMed=6089186;
 RA Takahashi N., Noma T., Honjo T.;
 RT "Rearranged immunoglobulin heavy chain variable region (VH)
 RT pseudogene that deletes the second complementarity-determining
 RT region.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
 DR PIR: A02090; G2HUCS.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 19
 FT CHAIN 20 147 IG HEAVY CHAIN V-II REGION SESS.
 FT DOMAIN 20 118 V SEGMENT.
 FT DOMAIN 119 132 D SEGMENT.
 FT DOMAIN 133 147 J SEGMENT.
 FT NON_TER 147 147
 FT SEQUENCE 147 AA; 16323 MW; FCBCDB3D00FB6666 CRC64;
 Query Match 46.2%; Score 342.5; DB 1; Length 147;
 Best Local Similarity 53.9%; Pred. No. 2.9e-27;
 Matches 76; Conservative 16; Mismatches 44; Indels 5; Gaps 2;
 QY 1 MAVLVFLCLVAPPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYG--VYVVRQ 58
 DB 1 MKVLSLLYLLTAIPG-ILSDVQLQESGPGLVKPSQSLSTCTVSGFSLTSYG--VYVVRQ 58
 QY 59 PPGKLEWLVGVIWAGGTTNNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116
 DB 59 PPGKLEWLVGVIWAGGTTNNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116
 QY 59 PPGKLEWLVGVIWAGGTTNNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116
 DB 59 PPGKLEWLVGVIWAGGTTNNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116
 RESULT 13
 HV2B_HUMAN STANDARD; PRT; 120 AA.
 ID HV2B_HUMAN
 AC P01815;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-II REGION COR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=70258837; PubMed=5449120;
 RA Press E.M., Hogg N.M.;
 RT "The amino acid sequences of the Fd fragments of two human gamma-1
 RT heavy chains.";
 RL Biochem. J. 117:641-660(1970).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.
 DR PIR: A02089; GIHUCO.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 DR Immunoglobulin V region; Glycoprotein.
 KW MOD_RES 1 94 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 94
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .).
 FT NON_TER 120 120
 FT SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EEB98 CRC64;
 Query Match 46.0%; Score 341.5; DB 1; Length 120;
 Best Local Similarity 60.0%; Pred. No. 3e-27; Indels 17; Gaps 5;
 Matches 78; Conservative 11; Mismatches 11; Mismatches 77
 QY 20 QVQLQESGPGLVKPSQTLSTCTVSGFSLTSYG--VYVVRQPGKLEWLVGVIWAGGTTN 77
 DB 1 QVTLRESGPAVLVKPTQTLTCTCFSGFSLSTGTCVGVIRQPPGKLEWLVGVIWAGGTTN 77
 QY 78 YNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR-----GPPHAMKRGYAMVW 132
 DB 61 YNTSELTSLTISKDTSKNQVSLKSSVTAADTAVYYCAR-----AGY-MDVW 110
 QY 133 GQGLTVTVSS 142
 DB 111 GRGTPVTVSS 120
 RESULT 14
 HV3J_HUMAN STANDARD; PRT; 121 AA.
 ID HV3J_HUMAN
 AC P01771;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-II REGION HIL.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE
RX MEDLINE=79124695; PubMed=420800;
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
RL cryoimmunoglobulin IgG Hil.";
RL Biochemistry 18:553-560(1979).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
DR PIR; A02054; GLHUHL.
DR HSP; P01772; 2IG2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
MOD_RES 1 Immunoglobulin V region.
NON_TER 121 121 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match 45.7%; Score 339; DB 1; Length 121;
Best Local Similarity 50.0%; Pred No. 5.3e-27;
Matches 62; Conservative 27; Mismatches 31; Indels 4; Gaps 2;
QY 20 QVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGIVYVRRQPPKGLVGLVWAGGT-TNY 78
Db 1 QVQLVAGGQVQPGKSLKSLASGFTFSYGMHWVRQAPGKGLVWVAVIYNGSTYY 60
QY 79 NSALMSRLTISKDTSKNOVSLKLSVTAADTAVYVCARGPPHAMKRGYAMDYWGQTLV 138
Db 61 GDSVGRFTISRDNSKRTLMZNSLRTEADTAVYICARDEPD---ILTAFSFDYWGQGLV 117
QY 139 TVSS 142
Db 118 TVSS 121

RESULT 15
ID HV3K_HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V-III REGION KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RL structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.*;
RN [2]
RP Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RL immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
J. Mol. Biol. 141:369-391(1980).
DR PIR; A02055; GLHUKL.
DR PDB; 2F84; 12-JUL-89.
DR PDB; 2IG2; 12-JUL-89.
DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; 3D-structure.
FT MOD_RES 1
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 113
FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 44.8%; Score 332.5; DB 1; Length 126;
Best Local Similarity 50.8%; Pred No. 2.4e-26;
Matches 64; Conservative 21; Mismatches 38; Indels 3; Gaps 2;
QY 20 QVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGIVYVRRQPPKGLVGLVWAGGT-TNY 78
Db 1 QVQLVAGGQVQPGKSLKSLASGFTFSYGMHWVRQAPGKGLVWVAVIYNGSTYY 60
QY 79 NSALMSRLTISKDTSKNOVSLKLSVTAADTAVYVCARGPPHAMKRGYAMDYWGQTLV 136
Db 61 GDSVGRFTISRDNSKRTLMZNSLRTEADTAVYICARDEPD---ILTAFSFDYWGQGLV 120
QY 137 TVSS 142
Db 121 TVSS 126

Search completed: May 7, 2002, 12:08:53
Job time: 451 sec

